

From: Romeo, David
Sent: Sunday, January 09, 2005 7:46 AM
To: STIC-Biotech/ChemLib
Subject: 10028051

Requester's Name: ... David Romeo
Serial Number: ... 10028051
Art Unit: ... 1647
Office: ... REM 4D39
Mailbox: ... REM 4C70
Phone: ... 571 272-0890
Date of Request: ... 01/09/05

PLEASE PROVIDE RESULTS ON DISK(s)

Search the commercial/public and interference files for SEQ ID NO: 1.

Search the commercial/public and interference files for SEQ ID NO: 3.

Search the commercial/public and interference files for SEQ ID NO: 23.

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Searcher: ED HART
Searcher Phone: 2-
Date Searcher Picked up: 1/10/05
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Searcher Prep/Rev. Time: 1/11/05
Online Time: _____

Type of Search

NA Sequence: # 3
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 066
WWW/Internet: _____
Other(Specify): _____

OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 9805.83 Seconds
(without alignments)
1148.874 Million cell updates/sec

Title: US-10-028-051A-1
Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcgcacg.....aaaaaaaaaaaaaaaa 2374

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_pa:*
2: gb_hhg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ote:*
12: gb_ey:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2335	98.4	2351	4	BTU24164
2	1467.4	61.8	2039	6	ARI29187
3	1467.4	61.8	2039	6	ARI47852
4	1399.6	59.0	1920	6	BD192740
5	1384.6	58.3	1909	6	AX329773
6	1384.6	58.0	1893	6	HSU1903
7	1376.4	58.0	1893	6	ARI16408
8	1376.4	58.0	1893	6	BD195148
9	1376.4	58.0	1893	6	HSU68057
10	1122.8	47.3	1476	6	AX565712
11	1122.8	47.3	1476	6	AX597112
12	1122.8	47.3	1476	6	AX701367
13	1122.8	47.3	1476	6	AX821908
14	1122.8	47.3	1476	6	HSU24163
15	1082.4	45.6	2814	10	BC016884
16	1070	45.1	2540	10	MMU8566
17	1055.2	44.4	1687	9	AK130009
18	1054.4	44.4	1363	9	BC027855
19	1034.2	43.6	2176	6	ARI16407

20	1034.2	43.6	2176	6	AX305981	AX305981 Sequence
21	1034.2	43.6	2176	10	MMU68058	U68058 Mus musculus
22	1031	43.4	2176	6	BD195147	BD195147 Endoderm,
23	831.8	35.0	1786	10	MMU91905	U91905 Mus musculus
24	676.6	28.5	124720	9	AC105396	AC105396 Homo sapi
25	672.8	28.3	1833	5	AF218057	AF218057 Gallus ga
26	654.6	27.6	207061	2	AC012552	AC012552 Homo sapi
27	607.2	25.6	1076	10	MAU91904	U91904 Mesocricetu
28	589	24.8	97944	9	AC108514	AC108514 Homo sapi
29	587	24.7	725	6	CQ719712	CQ719712 Sequence
30	481.6	20.3	640	5	AF207665	AF207665 Gallus ga
31	463.8	19.5	1867	5	BC074538	BC074538 Xenopus t
32	452.8	19.1	67845	2	AC016315	AC016315 Homo sapi
33	452	19.0	1291	5	XLU78598	U78598 Xenopus lae
34	447	18.8	190906	10	AL928578	AL928578 Mouse DNA
35	447	18.8	250663	2	AC134905	AC134905 Mus muscu
36	446	18.8	1875	5	U68059	U68059 Xenopus lae
37	446	18.8	1875	6	ARI16405	ARI16405 Sequence
38	446	18.8	1875	6	BD195145	BD195145 Endoderm,
39	420.8	17.7	611	11	BV099134	BV099134 RPRMSEGO
40	420.8	17.7	611	11	BV158572	BV158572 RPRMSEGO
41	415.4	17.5	238965	2	AC126647	AC126647 Rattus no
42	414.6	17.5	487	6	CQ691410	CQ691410 Sequence
43	413.6	17.4	1434	5	XLUJ3304	AU093304 Xenopus l
44	397.6	16.7	948	5	AF116853	AF116853 Danio rer
45	358.6	15.1	391	4	AB073103	AB073103 Oryctolag

OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 1036 Seconds
(without alignments)
12029.047 Million cell updates/sec

Title: US-10-028-051A-1
Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcgcacg.....aaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N GeneSeq_23Sep04:*
1: GeneSeqn1980a:*
2: GeneSeqn1990a:*
3: GeneSeqn2000a:*
4: GeneSeqn2001a:*
5: GeneSeqn2001ba:*
6: GeneSeqn2002a:*
7: GeneSeqn2002ba:*
8: GeneSeqn2003a:*
9: GeneSeqn2003ba:*
10: GeneSeqn2003ca:*
11: GeneSeqn2003da:*
12: GeneSeqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result- No.	Score	Query Match	Length	DB	ID	Description
1	2374	100.0	2374	2	AAV18253	Aav18253 Bovine gr
2	1467.4	61.8	2039	4	AAf80535	Aaf80535 Receptor
3	1467.4	61.8	2039	8	ABX77516	Abx77516 Different
4	1467.4	61.8	2039	12	ADL12749	Adl12749 Human ste
5	1399.6	59.0	1920	2	AAx28653	Aax28653 Nucleotid
6	1399.6	59.0	1920	3	AAA40573	Aaa40573 Xenopus s
7	1384.6	58.3	1909	2	AAV13101	Aav13101 Human haf
8	1384.6	58.3	1909	6	ABL61945	Ab161945 Colon ade
9	1384.6	58.3	1909	6	ABK64750	Abk64750 Human ben
10	1384.6	58.3	1909	10	ADL13671	Adl13671 Osteoarth
11	1384.6	58.3	1909	12	ADG20468	Adp20468 Human Fri
12	1384.6	58.3	1909	12	ADP21354	Adp21354 Gene FRZB
13	1376.4	58.0	1893	2	AAV14017	Aav14017 Human "fr
14	1124.4	47.4	1484	2	AAV18254	Aav18254 Human gro
15	1124.8	47.3	1476	8	ABX75332	Abx75332 Human CDN
16	1122.8	47.3	1476	8	AAD52561	Aad52561 FRZB DNA.
17	1122.8	47.3	1476	8	ABZ81833	Abz81833 SARP-2 nu
18	1122.8	47.3	1476	10	ADR66946	Adk66946 Gene #36
19	1070	45.1	2540	12	ADG20470	Adg20470 Mouse Fri
20	1034.2	43.6	2176	2	AAV14016	Aav14016 Mouse "fr
21	1034.2	43.6	2176	6	AB199691	Ab199691 Mouse lac
22	858	36.1	978	10	ADL13672	Adl13672 Osteoarth
23	831.8	35.0	1786	2	AAV13102	Aav13102 Mouse haf
24	831.8	35.0	2441	2	AAV13104	Aav13104 Mouse haf
25	607.2	25.6	1076	2	AAV13100	Aav13100 Hamster B
26	452	19.0	1291	2	AAV18255	Aav18255 Xenopus g
27	446	18.8	1875	2	AAV14014	Aav14014 Xenopus "
28	424.6	17.9	5301	2	AAV13105	Aav13105 Mouse haf
29	424.6	17.9	5355	2	AAV13103	Aav13103 Mouse haf
30	394	16.6	475	9	ACH13647	Ach13647 Human adu
31	313.4	13.2	1041	2	AAA99046	Aaa99046 Bos tauru
32	310.2	13.1	1046	2	AAx28655	Aax28655 Nucleotid
33	310.2	13.1	1581	2	AAx28656	Aax28656 Full leng
34	310.2	13.1	1767	4	AAc84495	Aac84495 Human FRA
35	308.6	13.0	1458	2	AAV08951	Aav08951 Human ARG
36	308.6	13.0	1767	2	AAV80657	Aav80657 Human FRA
37	308.6	13.0	1988	9	ADA24512	Ada24512 Human CDN
38	308.6	13.0	2009	4	AAf80598	Aaf80598 Receptor
39	306.4	12.9	2819	8	AAD52571	Aad52571 SRFP 4 DN
40	305.4	12.9	1041	3	AAA54128	Aaa54128 Breast ca
41	305.4	12.9	2820	6	ABK92118	Abk92118 Prostate
42	305.4	12.9	2820	8	ABZ34846	Abz34846 Coding se
43	305.4	12.9	2820	8	ABX76341	Abx76341 Lung canc
44	305.4	12.9	2820	8	ABX75341	Abx75341 Human CDN
45	305.4	12.9	2820	8	ABZ81843	Abz81843 SRFP-1 nu

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 208.86 Seconds
(without alignment)
8079.143 Million cell updates/sec

Title: US-10-028-051A-1
Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcgcag.....aaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptcdat/1/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptcdat/1/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptcdat/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptcdat/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptcdat/1/ina/PTCDS_COMB.seq:*
 - 6: /cgn2_6/ptcdat/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1467.4	61.8	2039	3	US-09-276-531-45	Sequence 45, Appl
2	1467.4	61.8	2039	4	US-09-976-594-478	Sequence 478, App
3	1376.4	58.0	1893	3	US-08-878-474-10	Sequence 10, Appl
4	1034.2	43.6	2176	3	US-08-878-474-8	Sequence 8, Appl
5	446	18.8	1875	3	US-08-878-474-4	Sequence 4, Appl
6	308.6	13.0	2009	3	US-09-276-531-108	Sequence 108, App
7	209.4	8.8	246	4	US-09-016-434-103	Sequence 103, App
8	72	3.0	401	4	US-09-643-597-277	Sequence 277, App
9	72	3.0	401	4	US-09-480-884A-277	Sequence 277, App
10	72	3.0	401	4	US-09-542-615A-277	Sequence 277, App
11	72	3.0	401	4	US-09-606-421B-277	Sequence 277, App
12	72	3.0	401	4	US-09-630-940B-277	Sequence 277, App
13	61.4	2.6	588	4	US-09-546-043-10	Sequence 10, Appl
14	61.4	2.6	1984	4	US-08-937-067-5	Sequence 5, Appl
15	58.4	2.5	741	4	US-09-546-043-11	Sequence 11, Appl
16	58.4	2.5	804	4	US-09-546-043-12	Sequence 12, Appl
17	58.4	2.5	942	4	US-09-546-043-9	Sequence 9, Appl
18	58.4	2.5	1017	4	US-09-546-043-2	Sequence 2, Appl
19	58.4	2.5	2075	4	US-09-087-031E-2	Sequence 2, Appl
20	58.4	2.5	2075	4	US-09-546-043-1	Sequence 1, Appl
21	58.4	2.5	2075	4	US-09-514-885-2	Sequence 2, Appl
22	58.4	2.5	2078	4	US-09-087-031E-1	Sequence 1, Appl
23	58.4	2.5	4245	3	US-09-276-531-16	Sequence 16, Appl
24	58.4	2.5	4500	4	US-09-087-031E-27	Sequence 27, Appl
25	56.8	2.4	1308	4	US-08-937-067-18	Sequence 18, Appl
26	55.2	2.3	1869	4	US-09-148-545-16	Sequence 56, Appl
27	54.6	2.3	870	4	US-08-937-067-3	Sequence 3, Appl
28	54.6	2.3	1960	4	US-09-148-545-114	Sequence 114, App
29	54.4	2.3	1141	4	US-09-806-708B-22	Sequence 22, Appl
30	49.4	2.1	7218	1	US-08-232-463-14	Sequence 14, Appl
31	49.2	2.1	2030	4	US-08-937-067-1	Sequence 1, Appl
32	45.2	1.9	2124	4	US-09-087-031E-26	Sequence 26, Appl
33	45	1.9	221	4	US-09-621-976-13585	Sequence 13585, A
34	45	1.9	1796	3	US-09-276-531-113	Sequence 113, App
35	45	1.9	2186	4	US-09-360-545-66	Sequence 66, Appl
36	44.4	1.9	1305	4	US-08-815-763-3	Sequence 3, Appl
37	44.4	1.9	1430	4	US-09-157-864-3	Sequence 3, Appl
38	44.2	1.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
39	44.2	1.9	11558	5	PCT-US93-06251-23	Sequence 23, Appl
40	44	1.9	1401	4	US-09-252-991A-14814	Sequence 14814, A
41	44	1.9	1908	4	US-09-252-991A-15075	Sequence 15075, A
42	44	1.9	3900	4	US-09-252-991A-14550	Sequence 14550, A
43	43.6	1.8	1383	4	US-09-735-846-1	Sequence 1, Appl
44	43.4	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
45	43.2	1.8	1008	4	US-09-780-641-1	Sequence 1, Appl

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 2258.27 Seconds
(without alignments)
6031.844 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcacg.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	1:	/cgn2_6/ptcodata/1/pubpna/US07_PUBCOMB.seq.*
	2:	/cgn2_6/ptcodata/1/pubpna/PCT_NEW_PUB.seq.*
	3:	/cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq.*
	4:	/cgn2_6/ptcodata/1/pubpna/US06_PUBCOMB.seq.*
	5:	/cgn2_6/ptcodata/1/pubpna/US07_NEW_PUB.seq.*
	6:	/cgn2_6/ptcodata/1/pubpna/PCTUS_PUBCOMB.seq.*
	7:	/cgn2_6/ptcodata/1/pubpna/US08_NEW_PUB.seq.*
	8:	/cgn2_6/ptcodata/1/pubpna/US08_PUBCOMB.seq.*
	9:	/cgn2_6/ptcodata/1/pubpna/US09A_PUBCOMB.seq.*
	10:	/cgn2_6/ptcodata/1/pubpna/US09B_PUBCOMB.seq.*
	11:	/cgn2_6/ptcodata/1/pubpna/US09C_PUBCOMB.seq.*
	12:	/cgn2_6/ptcodata/1/pubpna/US09_NEW_PUB.seq.*
	13:	/cgn2_6/ptcodata/1/pubpna/US10A_PUBCOMB.seq.*
	14:	/cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq.*
	15:	/cgn2_6/ptcodata/1/pubpna/US10C_PUBCOMB.seq.*
	16:	/cgn2_6/ptcodata/1/pubpna/US10D_PUBCOMB.seq.*
	17:	/cgn2_6/ptcodata/1/pubpna/US10E_PUBCOMB.seq.*
	18:	/cgn2_6/ptcodata/1/pubpna/US10_NEW_PUB.seq.*
	19:	/cgn2_6/ptcodata/1/pubpna/US11_NEW_PUB.seq.*
	20:	/cgn2_6/ptcodata/1/pubpna/US60_NEW_PUB.seq.*
	21:	/cgn2_6/ptcodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2374	100.0	2374	13	US-10-028-049-1
2	2374	100.0	2374	14	US-10-090-049-1
3	2374	100.0	2374	15	US-10-014-055-1
4	1493	62.9	2625	16	US-10-062-674-1395
5	1467.4	61.8	2039	9	US-09-974-298-16
6	1384.6	58.3	1909	10	US-09-960-706-989
7	1384.6	58.3	1909	10	US-09-873-319-645
8	1384.6	58.3	1909	10	US-09-873-367C-282
9	1376.4	58.0	1893	9	US-09-903-180B-10
10	1376.4	58.0	1893	9	US-09-903-187A-10
11	1376.4	58.0	1893	9	US-09-903-171A-10
12	1376.4	58.0	1893	9	US-09-903-188A-10
13	1376.4	58.0	1893	9	US-09-903-323A-10
14	1376.4	58.0	1893	9	US-09-903-325A-10
15	1376.4	58.0	1893	9	US-09-903-170C-10
16	1124.4	47.4	1484	13	US-10-028-051-3
17	1124.4	47.4	1484	14	US-10-090-049-3

18	1124.4	47.4	1484	15	US-10-014-055-3	Sequence 3, Appli
19	1122.8	47.3	1476	15	US-10-172-118-614	Sequence 614, App
20	1122.8	47.3	1476	16	US-10-342-887-614	Sequence 614, App
21	1034.2	43.6	2176	9	US-09-903-180B-8	Sequence 8, Appli
22	1034.2	43.6	2176	9	US-09-903-187A-8	Sequence 8, Appli
23	1034.2	43.6	2176	9	US-09-903-171A-8	Sequence 8, Appli
24	1034.2	43.6	2176	9	US-09-903-188A-8	Sequence 8, Appli
25	1034.2	43.6	2176	9	US-09-903-323A-8	Sequence 8, Appli
26	1034.2	43.6	2176	9	US-09-903-325A-8	Sequence 8, Appli
27	1034.2	43.6	2176	9	US-09-903-170C-8	Sequence 8, Appli
28	452	19.0	1291	13	US-10-028-051-23	Sequence 23, Appli
29	452	19.0	1291	14	US-10-090-049-23	Sequence 23, Appli
30	452	19.0	1291	15	US-10-014-055-23	Sequence 23, Appli
31	446	18.8	1875	9	US-09-903-180B-4	Sequence 4, Appli
32	446	18.8	1875	9	US-09-903-187A-4	Sequence 4, Appli
33	446	18.8	1875	9	US-09-903-171A-4	Sequence 4, Appli
34	446	18.8	1875	9	US-09-903-188A-4	Sequence 4, Appli
35	446	18.8	1875	9	US-09-903-323A-4	Sequence 4, Appli
36	446	18.8	1875	9	US-09-903-325A-4	Sequence 4, Appli
37	446	18.8	1875	9	US-09-903-170C-4	Sequence 4, Appli
38	414.6	17.5	487	16	US-10-242-535A-36336	Sequence 36336, A
39	414.6	17.5	487	16	US-10-085-783A-36336	Sequence 36336, A
40	394	16.6	475	10	US-09-918-995-859	Sequence 859, App
41	377.4	15.9	512	16	US-10-062-674-230	Sequence 230, App
42	333.2	14.0	574	16	US-10-242-535A-14020	Sequence 14020, A
43	333.2	14.0	574	16	US-10-085-783A-14020	Sequence 14020, A
44	325.2	13.7	492	15	US-10-102-524-1581	Sequence 1581, Ap
45	311.4	13.1	472	16	US-10-242-535A-42387	Sequence 42387, A

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 6773.9 Seconds
(without alignments)
12770.772 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcacg.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	1:	gb_est1.*
	2:	gb_est2.*
	3:	gb_hic.*
	4:	gb_est3.*
	5:	gb_est4.*
	6:	gb_est5.*
	7:	gb_est6.*
	8:	gb_ges1.*
	9:	gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1403.6	59.1	1891	3	CR622855	CR622855 full-length
2	1319.4	55.6	1780	3	CR620343	CR620343 full-length
3	1089.6	45.9	2922	3	AK029941	AK029941 Mus muscu
4	1084.6	45.7	2390	3	AK019093	AK019093 Mus muscu
5	1038.2	43.7	1305	3	CR593578	CR593578 full-length
6	889.8	37.5	1159	1	AL515416	AL515416 AL515416
7	818	34.5	1094	1	AL528836	AL528836 AL528836
8	817.4	34.4	1032	1	AL546734	AL546734 AL546734
9	805.8	33.9	1001	1	AL548498	AL548498 AL548498
10	774.6	32.6	1065	7	U69182	U69182 U69182 Soar
11	752.6	31.7	928	1	AL527859	AL527859 AL527859
12	748.4	31.5	750	7	CK775692	CK775692 966826 MA
13	745.8	31.4	1051	1	AL573040	AL573040 AL573040
14	740.2	31.2	991	1	AL526385	AL526385 AL526385
15	720.6	30.4	891	6	CD105319	CD105319 AGENCOURT
16	704.8	29.7	747	7	CR453950	CR453950 CR453950
17	661	27.8	797	9	AY410028	AY410028 Homo sapi
18	651	27.4	835	4	BI913036	BI913036 603179601
19	644.8	27.2	728	4	BI832471	BI832471 603082261
20	642.2	27.1	787	1	AU141161	AU141161 AU141161
21	640.6	27.0	1043	5	BX459201	BX459201 BX459201
22	638.4	26.9	730	5	BP147378	BP147378 BP147378
23	638.2	26.9	745	5	BP148017	BP148017 BP148017
24	635.8	26.8	719	7	CN315376	CN315376 170004245
25	629.4	26.5	712	5	BX955693	BX955693 DKFZP781C
26	622	26.2	805	5	BI769191	BI769191 603060007
27	617.8	26.0	714	5	BP455757	BP455757 BP455757
28	608.8	25.6	1010	1	AL526570	AL526570 AL526570
29	608.2	25.6	797	9	AY410030	AY410030 Mus muscu
30	601.6	25.3	829	7	CF411660	CF411660 CH34075 B
31	596.2	25.1	1106	1	AL546699	AL546699 AL546699
32	592.2	24.9	678	2	AW160750	AW160750 aw75f01.Y
33	591.6	24.9	797	9	AY410029	AY410029 Pan trogl
34	590.8	24.9	667	7	CN315375	CN315375 170004246
35	587.6	24.8	1182	1	AL528835	AL528835 AL528835
36	585	24.6	680	4	BI761532	BI761532 603046682
37	578.6	24.4	940	5	BU409451	BU409451 603157994
38	573	24.1	584	5	BM253949	BM253949 515238 MA
39	571	24.1	740	1	AU117730	AU117730 AU117730
40	568.2	23.9	658	5	BP152493	BP152493 BP152493
41	566.8	23.9	789	5	B0852855	B0852855 AGENCOURT
42	565.8	23.8	658	6	CA773784	CA773784 lm57a11.Y
43	551.2	23.2	629	5	BX955707	BX955707 DKFZP781D
44	550.2	23.2	624	6	CB160361	CB160361 K-EST0220
45	549.4	23.1	551	4	BM031987	BM031987 497568 MA

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OW nucleic - nucleic search, using BW model

Run on: January 10, 2005, 11:50:10 ; Search time 6129.68 Seconds
(without alignment)
11448.874 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 cggggccctggggcgggaaggg.....acatgctgttaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_rte.*
12: gb_ey.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1473	99.3	1476	6	AX565712	AX565712 Sequence
2	1473	99.3	1476	6	AX597112	AX597112 Sequence
3	1473	99.3	1476	6	AX701367	AX701367 Sequence
4	1473	99.3	1476	6	AX821908	AX821908 Sequence
5	1473	99.3	1476	6	HSU24193	U24163 Human Fritx
6	1464.4	98.7	2039	6	AR129187	AR129187 Sequence
7	1464.4	98.7	2039	6	AR447852	AR447852 Sequence
8	1337	90.1	1363	9	BC027855	BC027855 Homo sapi
9	1326.6	89.4	1920	6	BD192740	BD192740 Secreted
10	1316.2	88.7	1893	6	AR116408	AR116408 Sequence
11	1316.2	88.7	1893	9	HSU68057	U68057 Human Fretz
12	1316.2	88.7	1893	9	AX329773	AX329773 Sequence
13	1314.6	88.6	1909	6	AX329773	U91903 Human Fritx
14	1314.6	88.6	1909	6	HSU91903	BD195148 Endoderm,
15	1124.4	75.8	2351	4	BTU24164	BTU24164
16	974.6	65.7	1687	9	AK130009	AK130009 Homo sapi
17	860.6	58.0	2814	10	BC016884	BC016884 Mus muscu
18	846.6	57.0	2540	10	MMU88568	U88568 Mus muscu
19	842.8	56.8	1786	10	MMU91905	U91905 Mus muscu
20	832.8	56.1	2176	6	AR116407	AR116407 Sequence
21	832.8	56.1	2176	6	BD195147	BD195147 Endoderm,
22	832.8	56.1	2176	6	AX305981	AX305981 Sequence
23	832.8	56.1	2176	10	MMU68058	U68058 Mus muscu
24	670	45.1	97944	9	AC108514	AC108514 Homo sapi
25	667	44.9	725	6	CQ719712	CQ719712 Sequence
26	660	44.5	1833	5	AF218057	AF218057 Gallus ga
27	630.6	42.5	1076	10	MAU91904	U91904 Mesocricetu
28	483.4	32.6	487	6	CQ691410	CQ691410 Sequence
29	473.6	31.9	640	5	AF207665	AF207665 Gallus ga
30	466.4	31.4	1291	5	XLU78598	U78598 Xenopus lae
31	466.2	31.4	1867	5	BC074538	BC074538 Xenopus t
32	462	31.1	1875	5	U68059	U68059 Xenopus lae
33	462	31.1	1875	6	AR116405	AR116405 Sequence
34	462	31.1	1875	6	BD195145	BD195145 Endoderm,
35	452.6	30.5	472	6	CQ697461	CQ697461 Sequence
36	445.8	30.0	450	6	CQ683279	CQ683279 Sequence
37	436.6	29.4	190906	10	AL928578	AL928578 Mouse DNA
38	436.6	29.4	250663	2	AC134905	AC134905 Mus muscu
39	435.4	29.3	452	6	CQ685419	CQ685419 Sequence
40	434	29.2	611	11	BV099134	BV099134 RPAWMSBO

C	41	434	29.2	611	11	BV158572	BPV158572 RPAWMEQO
	42	423	28.5	1434	5	XLAV9304	AD009304 Xenopus 1
	43	419.6	28.3	23865	2	AC126647	AC126647 Rattus no
	44	412.4	27.8	427	6	CQ695880	CQ695880 Sequence
	45	410	27.6	124720	9	AC105396	AC105396 Homo sapi

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 647.611 Seconds
(without alignment)
12029.047 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484
Sequence: 1 cgs9gacctgsgcgsgaagsgg9.....acatgctgttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: Geneseqn1980a:*
2: Geneseqn1990a:*
3: Geneseqn2000a:*
4: Geneseqn2001a:*
5: Geneseqn2002a:*
6: Geneseqn2003a:*
7: Geneseqn2003a:*
8: Geneseqn2003a:*
9: Geneseqn2003a:*
10: Geneseqn2003c:*
11: Geneseqn2003d:*
12: Geneseqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1483.6	100.0	1484	2	AAV18254	Aav18254 Human gro
	2	1473	99.3	1476	8	ABX75332	Abx75332 Human cdn
	3	1473	99.3	1476	8	AAD52561	Aad52561 FRZB DNA.
	4	1473	99.3	1476	8	AB281833	Ab281833 SARP-2 nu
	5	1473	99.3	1476	10	ADK66946	Adk66946 Gene #36
	6	1464.4	98.7	2039	4	AAF80535	Aaf80535 Receptor
	7	1464.4	98.7	2039	8	ABX77516	Abx77516 Different
	8	1464.4	98.7	2039	12	ADL12749	Adl12749 Human ate
	9	1326.6	89.4	1920	2	AAx28653	Aax28653 Nucleotid
	10	1326.6	89.4	1920	3	AAA40573	Aaa40573 Xenopus s
	11	1316.2	88.6	1909	2	AAV14017	Aav14017 Human "fr
	12	1314.6	88.6	1909	6	AB161945	Ab161945 Colon ade
	13	1314.6	88.6	1909	6	ABK64750	Abk64750 Human ben
	14	1314.6	88.6	1909	10	ADL13671	Adl13671 Osteoarth
	15	1314.6	88.6	1909	12	ADG20468	Adg20468 Human Fri
	16	1314.6	88.6	1909	12	ADG20468	Adg20468 Human Fri

	17	1314.6	88.6	1909	12	ADP21354	Adp21354 Gene FRZB
	18	1124.4	75.8	2374	2	AAV18253	Aav18253 Bovine gr
	19	976.4	65.8	978	10	ADL13672	Adl13672 Osteoarth
	20	846.6	57.0	2540	12	ADG20470	Adg20470 Mouse Fir
	21	844.8	56.9	2441	2	AAV13104	Aav13104 Mouse haf
	22	842.8	56.8	1786	2	AAV13102	Aav13102 Mouse haf
	23	832.8	56.1	2176	2	AAV14016	Aav14016 Mouse "fr
	24	832.8	56.1	2176	6	AB199691	Ab199691 Mouse ioc
	25	630.6	42.5	1076	6	AAV13100	Aav13100 Hamster B
	26	470.2	31.7	476	6	ABK64764	Abk64764 Human ben
	27	466.4	31.4	1291	2	AAV18255	Aav18255 Xenopus g
	28	462	31.1	1875	2	AAV14014	Aav14014 Xenopus "
	29	435.6	29.4	475	9	ACH13647	Ach13647 Human adu
	30	419.6	28.3	5301	2	AAV13105	Aav13105 Mouse haf
	31	419.6	28.3	5355	2	AAV13103	Aav13103 Mouse haf
	32	407.2	27.4	489	9	ACH28855	Ach28855 Human adu
	33	392.6	19.7	1041	3	AAx99046	Aax99046 Bos tauru
	34	289.4	19.5	1458	2	AAV08951	Aav08951 Human ATG
	35	289.4	19.5	1988	9	ADA24512	Ada24512 Human cdn
	36	289.4	19.5	2009	4	AAF80598	Aaf80598 Receptor
	37	288.8	19.5	2819	8	AAD52571	Aad52571 SRFP 4 DN
	38	287.8	19.4	1046	2	AAx28655	Aax28655 Nucleotid
	39	287.8	19.4	1581	2	AAx28656	Aax28656 Full leng
	40	287.8	19.4	1767	4	AAc84495	Aac84495 Human FRA
	41	286.2	19.3	1041	3	AAA54128	Aaa54128 Breast ca
	42	286.2	19.3	1767	2	AAV80657	Aav80657 Human FRA
	43	286.2	19.3	2820	6	ABK92118	Abk92118 Prostate
	44	286.2	19.3	2820	8	AB234846	Ab234846 Coding se
	45	286.2	19.3	2820	8	ABX76341	Abx76341 Lung canc

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OM nucleic - nucleic search, using sw model
Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds
(without alignment)
8079.143 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 cgs9gacctgsgcgsgaagsgg9.....acatgctgttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/6C_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match Length	DB	ID	Description
1	1464.4	98.7	2039	3 US-09-276-531-45	Sequence 45, Appl
2	1464.4	98.7	2039	4 US-09-976-594-478	Sequence 107, App
3	1316.2	88.7	1893	3 US-08-878-474-10	Sequence 10, Appl
4	832.8	56.1	2176	3 US-08-878-474-8	Sequence 8, Appl
5	462	31.1	1875	3 US-08-878-474-4	Sequence 4, Appl
6	289.4	19.5	2009	3 US-09-276-531-108	Sequence 108, App
7	235	15.8	246	4 US-09-016-434-103	Sequence 103, App
8	64	4.3	401	4 US-09-643-597-277	Sequence 277, App
9	64	4.3	401	4 US-09-480-884A-277	Sequence 277, App
10	64	4.3	401	4 US-09-542-615A-277	Sequence 277, App
11	64	4.3	401	4 US-09-606-421B-277	Sequence 277, App
12	64	4.3	401	4 US-09-630-940B-277	Sequence 277, App
13	61.4	4.1	588	4 US-09-546-043-10	Sequence 10, Appl
14	61.4	4.1	1984	4 US-08-937-067-5	Sequence 5, Appl
15	59	4.0	741	4 US-09-546-043-11	Sequence 11, Appl
16	59	4.0	804	4 US-09-546-043-12	Sequence 12, Appl
17	59	4.0	942	4 US-09-546-043-2	Sequence 2, Appl
18	59	4.0	1017	4 US-09-546-043-9	Sequence 9, Appl
19	59	4.0	2075	4 US-09-087-031E-2	Sequence 2, Appl
20	59	4.0	2075	4 US-09-546-043-1	Sequence 1, Appl
21	59	4.0	2075	4 US-09-514-885-2	Sequence 2, Appl
22	59	4.0	2078	4 US-09-087-031E-1	Sequence 1, Appl
23	59	4.0	4245	3 US-09-276-531-16	Sequence 16, Appl
24	59	4.0	4500	4 US-09-087-031E-27	Sequence 27, Appl
25	57.4	3.9	1308	4 US-08-937-067-18	Sequence 18, Appl
26	51.8	3.5	1869	4 US-09-148-545-56	Sequence 56, Appl
27	51.2	3.5	870	4 US-08-937-067-3	Sequence 3, Appl
28	51.2	3.5	1960	4 US-09-148-545-114	Sequence 114, App
29	49	3.2	2030	4 US-08-937-067-1	Sequence 1, Appl
30	46.8	3.2	6090	4 US-09-631-603-1	Sequence 1, Appl
31	45.8	3.1	7218	1 US-08-232-463-14	Sequence 14, Appl
32	45.2	3.0	546	4 US-09-252-991A-6912	Sequence 6912, Ap
33	45.2	3.0	1197	4 US-09-252-991A-6737	Sequence 6737, Ap
34	45.2	3.0	1272	4 US-09-252-991A-6952	Sequence 6952, Ap
35	45.2	3.0	2346	4 US-09-252-991A-6782	Sequence 6782, Ap
36	44.6	3.0	2124	4 US-09-087-031E-26	Sequence 26, Appl
37	43	2.9	711	4 US-09-252-991A-5727	Sequence 5727, Ap
38	43	2.9	765	4 US-09-252-991A-15854	Sequence 15854, A
39	43	2.9	1548	4 US-09-252-991A-5713	Sequence 5713, Ap
40	43	2.9	1971	4 US-09-252-991A-5699	Sequence 5699, Ap
41	43	2.9	2265	4 US-09-252-991A-5738	Sequence 5738, Ap
42	42.8	2.9	2310	3 US-08-956-182-13	Sequence 13, Appl
43	42.8	2.9	7218	1 US-08-232-463-14	Sequence 14, Appl
44	42.4	2.9	1446	4 US-09-252-991A-10586	Sequence 10586, A
45	42.4	2.9	3222	4 US-09-252-991A-10770	Sequence 10770, A

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 1411.66 Seconds
(without alignment)
6031.844 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 cggggcctgggcggaaggggg.....acatgctgtaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1483.6	100.0	1484	13 US-10-028-051-3	Sequence 3, Appl
2	1483.6	100.0	1484	14 US-10-090-049-3	Sequence 3, Appl
3	1483.6	100.0	1484	15 US-10-014-055-3	Sequence 3, Appl
4	1473	99.3	1476	15 US-10-172-118-614	Sequence 614, App
5	1473	98.3	1476	16 US-10-342-887-614	Sequence 614, App
6	1464.4	99.7	2039	9 US-09-974-298-16	Sequence 16, Appl
7	1427.2	96.2	2625	16 US-10-062-674-1395	Sequence 1395, Ap
8	1316.2	88.7	1893	9 US-09-903-180B-10	Sequence 10, Appl
9	1316.2	88.7	1893	9 US-09-903-187A-10	Sequence 10, Appl
10	1316.2	88.7	1893	9 US-09-903-171A-10	Sequence 10, Appl
11	1316.2	88.7	1893	9 US-09-903-188A-10	Sequence 10, Appl
12	1316.2	88.7	1893	9 US-09-903-323A-10	Sequence 10, Appl
13	1316.2	88.7	1893	9 US-09-903-325A-10	Sequence 10, Appl
14	1316.2	88.6	1893	9 US-09-903-170C-10	Sequence 10, Appl
15	1314.6	88.6	1909	10 US-09-960-706-989	Sequence 989, App
16	1314.6	88.6	1909	10 US-09-873-319-645	Sequence 645, App
17	1314.6	88.6	1909	10 US-09-873-367C-282	Sequence 282, App
18	1124.4	75.8	2374	13 US-10-028-051-1	Sequence 1, Appl
19	1124.4	75.8	2374	14 US-10-090-049-1	Sequence 1, Appl
20	1124.4	75.8	2374	15 US-10-014-055-1	Sequence 1, Appl
21	832.8	56.1	2176	9 US-09-903-180B-8	Sequence 8, Appl
22	832.8	56.1	2176	9 US-09-903-187A-8	Sequence 8, Appl
23	832.8	56.1	2176	9 US-09-903-171A-8	Sequence 8, Appl
24	832.8	56.1	2176	9 US-09-903-188A-8	Sequence 8, Appl
25	832.8	56.1	2176	9 US-09-903-323A-8	Sequence 8, Appl
26	832.8	56.1	2176	9 US-09-903-325A-8	Sequence 8, Appl
27	832.8	56.1	2176	9 US-09-903-170C-8	Sequence 8, Appl
28	483.4	32.6	487	16 US-10-242-535A-36336	Sequence 36336, A
29	483.4	32.6	487	16 US-10-085-783A-36336	Sequence 36336, A
30	470.2	31.7	476	10 US-09-960-706-1006	Sequence 1006, App
31	470.2	31.7	476	10 US-09-873-319-659	Sequence 659, App
32	466.4	31.4	1291	13 US-10-028-051-23	Sequence 23, Appl
33	466.4	31.4	1291	14 US-10-090-049-23	Sequence 23, Appl
34	466.4	31.4	1291	15 US-10-014-055-23	Sequence 23, Appl
35	462	31.1	1875	9 US-09-903-180B-4	Sequence 4, Appl
36	462	31.1	1875	9 US-09-903-187A-4	Sequence 4, Appl
37	462	31.1	1875	9 US-09-903-171A-4	Sequence 4, Appl
38	462	31.1	1875	9 US-09-903-188A-4	Sequence 4, Appl

39	462	31.1	1875	9	US-09-903-323A-4	Sequence 4, Appli
40	462	31.1	1875	9	US-09-903-325A-4	Sequence 4, Appli
41	462	31.1	1875	9	US-09-903-170C-4	Sequence 4, Appli
42	452.6	30.5	472	16	US-10-242-535A-42387	Sequence 42387, A
43	452.6	30.5	472	16	US-10-085-783A-42387	Sequence 42387, A
44	445.8	30.0	450	16	US-10-242-535A-28205	Sequence 28205, A
45	445.8	30.0	450	16	US-10-085-783A-28205	Sequence 28205, A

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 4234.4 Seconds
(without alignments)
12770.772 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 CGG9GCGCTG9GCGAGG999.....acatgctgttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_sact1.*
2: gb_sact2.*
3: gb_hic.*
4: gb_sact3.*
5: gb_sact4.*
6: gb_sact5.*
7: gb_sact6.*
8: gb_g9981.*
9: gb_g9982.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330.2	89.6	1891	3	CR622855 full-leng
2	1298	87.5	1305	3	CR593578 full-leng
3	1259.2	84.9	1780	3	CR620343 full-leng
4	1040.6	70.1	1159	1	AL515416
5	1014.2	68.3	1065	7	U69182
6	963.2	64.9	1051	1	AL573040
7	939.8	63.3	1094	1	AL528836
8	937.4	63.2	1032	1	AL546734
9	923.6	62.2	1001	1	AL548498
10	875.6	59.0	991	1	AL526385
11	871.4	58.7	928	1	AL527859
12	861.4	58.0	2390	3	AK019093
13	861.4	58.0	2922	3	AK029941
14	814.4	54.9	891	6	CD105319
15	766.2	51.6	781	5	BQ044934
16	754.2	50.8	1043	5	BX459201
17	749	50.5	797	9	AY410028

c	18	739	49.8	762	5	B0182099
c	19	737.2	49.7	835	4	B1913036
c	20	731	49.3	739	5	BQ006836
c	21	730.4	49.2	789	5	B0852855
c	22	728	49.1	737	5	B0733641
c	23	725.4	48.9	787	1	AU141161
c	24	718	48.4	728	4	B1832471
c	25	713.2	48.1	805	4	B1769191
c	26	709	47.8	719	7	CN315376
c	27	700.8	47.2	712	5	BX955693
c	28	681.4	45.9	708	1	A1075764
c	29	676.6	45.6	740	1	AU117730
c	30	666.8	44.9	797	9	AY410029
c	31	665.6	44.9	693	5	B0732915
c	32	661.6	44.6	678	2	AW160750
c	33	659.8	44.5	695	1	A1983481
c	34	659	44.4	667	7	CN315375
c	35	653.8	44.1	680	4	B1761532
c	36	635.6	42.8	658	6	CA773784
c	37	632.2	42.6	797	9	AY410030
c	38	627.2	42.3	653	4	BM706252
c	39	625.8	42.2	745	5	BP148017
c	40	625	42.1	730	5	BP147378
c	41	624.6	42.1	705	2	AW955823
c	42	624.4	42.1	642	4	B1711161
c	43	616.2	41.5	629	5	BX955707
c	44	612	41.2	624	6	CB160361
c	45	610	41.1	641	4	B1668012

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 5332.49 Seconds
(without alignments)
11448.874 Million cell updates/sec

Title: US-10-028-051A-23

Perfect score: 1291

Sequence: 1 tttaactgtgcagctctccc.....agcctatcacctgataccta 1291

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenBank1.*
1: gb_ba.*
2: gb_hic.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_at.*
12: gb_ay.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1291	100.0	1291	5	XLU78598	U78598 Xenopus lae
2	1131.6	87.7	1875	5	U68059	U68059 Xenopus lae
3	1131.6	87.7	1875	6	AR116405	AR116405 Sequence
4	1131.6	87.7	1875	6	BD195145	BD195145 Endoderm,
5	1028.2	79.6	1867	5	BC074538	BC074538 Xenopus t
6	992.4	76.9	1434	5	XLAU9304	XLAU9304 Xenopus l
7	518	40.1	1833	5	AF218057	AF218057 Gallus ga
8	468	36.3	1920	6	BD192740	BD192740 Secreted
9	466.4	36.1	1363	9	BC027855	BC027855 Homo sapi
10	466.4	36.1	1893	6	AR116408	AR116408 Sequence
11	466.4	36.1	1893	6	BD195148	BD195148 Endoderm,
12	466.4	36.1	1893	9	HSU68057	HSU68057 Human firez
13	466.4	36.1	2039	6	AR129187	AR129187 Sequence
14	466.4	36.1	2039	6	AR447852	AR447852 Sequence
15	464.8	36.0	1476	6	AX565712	AX565712 Sequence
16	464.8	36.0	1476	6	AX597112	AX597112 Sequence
17	464.8	36.0	1476	6	AX701367	AX701367 Sequence
18	464.8	36.0	1476	6	AX821908	AX821908 Sequence
19	464.8	36.0	1476	9	HSU24163	HSU24163 Human Frliz
20	464.8	36.0	1909	9	AX329773	AX329773 Sequence
21	464.8	36.0	1909	9	HSU91903	HSU91903 Human Frliz
22	463.6	35.9	2814	10	BC016884	BC016884 Mus muscu
23	462	35.8	1786	10	MMU91905	MMU91905 Mus muscu
24	462	35.8	2176	6	AR116407	AR116407 Sequence
25	462	35.8	2176	6	BD195147	BD195147 Endoderm,
26	462	35.8	2176	6	AX305981	AX305981 Sequence
27	462	35.8	2176	10	MMU68058	MMU68058 Mus muscu
28	462	35.8	2540	10	MMU88568	MMU88568 Mus muscu
29	452	35.0	2351	4	BTU24164	BTU24164 Bos taurus
30	394.6	30.6	948	5	AF116853	AF116853 Danio rer
31	373.6	28.9	1076	10	MAU91904	MAU91904 Mesocricetu
32	373.4	28.9	640	5	AF207665	AF207665 Gallus ga
33	345.6	26.8	725	6	CQ719712	CQ719712 Sequence
34	283.6	22.0	1687	9	AK130009	AK130009 Homo sapi
35	266.6	20.7	1785	10	AF117709	AF117709 Mus muscu
36	263.4	20.4	1739	10	BC034853	BC034853 Mus muscu
37	259.8	20.1	97944	9	AC108514	AC108514 Homo sapi
38	258.6	20.0	19096	10	AL928578	AL928578 Mouse DNA
39	258.6	20.0	238965	2	AC126647	AC126647 Rattus no
40	258.6	20.0	250663	2	AC134905	AC134905 Mus muscu
41	257.2	19.9	611	11	BV099134	BV099134 RPAWMSQ
42	257.2	19.9	611	11	BV158572	BV158572 RPAWMSQ
43	251.8	19.5	1910	10	AF012891	AF012891 Rattus no
44	250.8	19.4	1715	10	AF140346	AF140346 Rattus no
45	247.6	19.2	162126	2	CR513785	CR513785 Danio rer

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 563.386 Seconds
(without alignment)
12029.047 Million cell updates/sec

Title: US-10-028-051A-23

Perfect score: 1291
Sequence: 1 ttctactgtgcagctctccc.....agcctatcattcgtacacta 1291

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	N_Geneseq_23Sep04:*
1:	geneseqn1960a:*
2:	geneseqn1990a:*
3:	geneseqn2000a:*
4:	geneseqn2001a:*
5:	geneseqn2001ba:*
6:	geneseqn2002a:*
7:	geneseqn2002ba:*
8:	geneseqn2003a:*
9:	geneseqn2003ba:*
10:	geneseqn2003ca:*
11:	geneseqn2003da:*
12:	geneseqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1291	100.0	1291	2	AAV18255	Aav18255 Xenopus g
2	1131.6	87.7	1875	2	AAV14014	Aav14014 Xenopus "
3	468	36.3	1920	2	AAx28653	Aax28653 Nucleotid
4	468	36.3	1920	3	AAA40573	Aaa40573 Xenopus s
5	466.4	36.1	1484	2	AAV18254	Aav18254 Human gro
6	466.4	36.1	1893	2	AAV14017	Aav14017 Human "fr
7	466.4	36.1	2039	4	AAF80535	Aaf80535 Receptor
8	466.4	36.1	2039	8	ABX77516	Abx77516 Different
9	466.4	36.1	2039	12	ADL12749	Adl12749 Human ste
10	464.8	36.0	1476	8	ABX75332	Abx75332 Human CDN
11	464.8	36.0	1476	8	AAD52561	Aad52561 FRZB DNA.
12	464.8	36.0	1476	8	ABZ81833	Abz81833 SARP-2 nu
13	464.8	36.0	1476	10	ADK66946	Adk66946 Gene #36
14	464.8	36.0	1909	2	AAV13101	Aav13101 Human ben
15	464.8	36.0	1909	6	ABL61945	Abi61945 Colon ade
16	464.8	36.0	1909	6	ABK64750	Abk64750 Human ben
17	464.8	36.0	1909	10	ADL13671	Adl13671 Osteoarth
18	464.8	36.0	1909	12	ADG20468	Adg20468 Human Frl
19	464.8	36.0	1909	12	ADP21354	Adp21354 Gene FRZB
20	462	35.8	1786	2	AAV13102	Aav13102 Mouse haf
21	462	35.8	2176	2	AAV14016	Aav14016 Mouse "fr
22	462	35.8	2176	6	AB199691	Abi199691 Mouse iac
23	462	35.8	2441	2	AAV13104	Aav13104 Mouse haf
24	462	35.8	2540	12	ADG20470	Adg20470 Mouse Frl
25	459.8	35.6	978	10	ADL13672	Adl13672 Osteoarth
26	452	35.0	2374	2	AAV18253	Aav18253 Bovine gr
27	373.6	28.9	1076	2	AAV13100	Aav13100 Hamster B
28	321.6	24.9	352	3	AAA43168	Aaa43168 Xenopus s
29	245.8	19.0	5301	2	AAV13105	Aav13105 Mouse haf
30	245.8	19.0	5355	2	AAV13103	Aav13103 Mouse haf
31	244.2	18.9	1458	2	AAV08951	Aav08951 Human ATG
32	244.2	18.9	1988	9	ADA24512	Ada24512 Human CDN
33	244.2	18.9	2009	4	AAF80598	Aaf80598 Receptor
34	241	18.7	1041	3	AAA54128	Aaa54128 Breast ca
35	241	18.7	1046	2	AAx28655	Aax28655 Nucleotid
36	241	18.7	1581	2	AAx28656	Aax28656 Full leng
37	241	18.7	1767	2	AAV80657	Aav80657 Human FRA
38	241	18.7	1767	4	AAc84495	Aac84495 Human FRA
39	241	18.7	2820	6	ABK92118	Abk92118 Prostate
40	241	18.7	2820	8	ABZ34846	Abz34846 Coding se

41 241 18.7 2820 8 ABX76341 ABX76341 Lung canc
42 241 18.7 2820 8 ABX75341 ABX75341 Human CDN
43 241 18.7 2820 8 AB281843 AB281843 SRFP-1 nu
44 241 18.7 2820 11 ADN38745 ADN38745 Cancer/an
45 241 18.7 2820 11 ADN39642 ADN39642 Cancer/an

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 113.58 Seconds
(without alignments)
8079.143 Million cell updates/sec

Title: US-10-028-051A-23

Perfect score: 1291

Sequence: 1 ttaccgtgcagctctccc.....agcctatcatctgataccta 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patente_NA:*
1: /cgm2_6/ptodaca/1/ina/5A_COMB.seq:*
2: /cgm2_6/ptodaca/1/ina/5B_COMB.seq:*
3: /cgm2_6/ptodaca/1/ina/6A_COMB.seq:*
4: /cgm2_6/ptodaca/1/ina/6B_COMB.seq:*
5: /cgm2_6/ptodaca/1/ina/PCRTUS_COMB.seq:*
6: /cgm2_6/ptodaca/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1131.6	87.7	1875	3	US-08-878-474-4
2	466.4	36.1	1893	3	US-08-878-474-10
3	466.4	36.1	2039	3	US-09-276-531-45
4	466.4	36.1	2039	4	US-09-276-531-45
5	462	35.8	2176	3	US-08-878-474-8
6	244.2	18.9	2009	3	US-09-276-531-108
7	107.6	8.3	246	4	US-09-016-434-103
8	70	5.4	401	4	US-09-643-597-277
9	70	5.4	401	4	US-09-480-884A-277
10	70	5.4	401	4	US-09-542-615A-277
11	70	5.4	401	4	US-09-606-421B-277
12	70	5.4	401	4	US-09-630-940B-277
13	56.6	4.4	1716	3	US-09-276-531-113
14	49.6	3.8	7218	1	US-08-232-463-14
15	42.4	3.3	1141	4	US-09-806-708B-22
16	35.6	2.8	1960	4	US-08-545-528D-1
17	35.4	2.7	580073	4	US-09-146-545-114
18	35.2	2.7	832	4	US-09-621-976-2813
19	35.2	2.7	1906	3	US-09-031-962D-5
20	35	2.7	1109	4	US-07-145-002B-31
21	35	2.7	1109	4	US-06-256-204C-31
22	35	2.7	1869	4	US-09-146-545-56

23	34.6	2.7	3436	4	US-09-919-039-277	Sequence 277, App
24	34.6	2.7	4069	4	US-09-620-312D-174	Sequence 174, App
25	34.6	2.7	202001	4	US-09-734-674-3	Sequence 3, Appl
26	34.4	2.7	561	4	US-09-248-796A-4855	Sequence 4855, Ap
27	34.2	2.6	1984	4	US-08-937-067-5	Sequence 5, Appl
28	34.2	2.6	2565	3	US-08-965-492-7	Sequence 7, Appl
29	34.2	2.6	3026	4	US-09-919-039-314	Sequence 314, App
30	34.2	2.6	8050	3	US-09-421-362-11	Sequence 11, Appl
31	34.2	2.6	8050	4	US-09-874-562-11	Sequence 11, Appl
32	34.2	2.6	1830121	4	US-09-557-884-1	Sequence 1, Appl
33	34.2	2.6	1830121	4	US-09-643-990A-1	Sequence 1, Appl
34	34.2	2.6	1830121	4	US-10-329-960-1	Sequence 1, Appl
35	34	2.6	1287	3	US-08-845-258-11	Sequence 11, Appl
36	34	2.6	1287	3	US-08-990-571-11	Sequence 11, Appl
37	34	2.6	1287	3	US-08-723-142A-11	Sequence 11, Appl
38	34	2.6	1287	4	US-09-528-784A-11	Sequence 11, Appl
39	34	2.6	1287	4	US-09-569-098A-11	Sequence 11, Appl
40	34	2.6	7218	1	US-08-232-463-14	Sequence 14, Appl
41	33.8	2.6	168575	4	US-09-426-290-1	Sequence 1, Appl
42	33.6	2.6	475	4	US-09-621-976-909	Sequence 909, Ap
43	33.6	2.6	501	4	US-09-328-352-439	Sequence 439, App
44	33.6	2.6	621	4	US-09-248-796A-7246	Sequence 7246, Ap
45	33.4	2.6	664	4	US-09-904-615-66	Sequence 66, Appl

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 128.07 Seconds
(without alignments)
6031.844 Million cell updates/sec

Title: US-10-028-051A-23
Perfect score: 1291
Sequence: 1 ttaccgtgcagctctccc.....agcctatcatctgataccta 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgm2_6/ptodaca/1/pubpna/US07_PUBCOMB.seq:*
2: /cgm2_6/ptodaca/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgm2_6/ptodaca/1/pubpna/US06_NEW_PUB.seq:*
4: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
5: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
6: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
7: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
8: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
9: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
10: /cgm2_6/ptodaca/1/pubpna/US06_PUBCOMB.seq:*
11: /cgm2_6/ptodaca/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgm2_6/ptodaca/1/pubpna/US09C_PUBCOMB.seq:*
13: /cgm2_6/ptodaca/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgm2_6/ptodaca/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgm2_6/ptodaca/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgm2_6/ptodaca/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgm2_6/ptodaca/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgm2_6/ptodaca/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgm2_6/ptodaca/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgm2_6/ptodaca/1/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pub/pbna/US60_PUBCOMB.seq:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1291	100.0	1291	13	US-10-028-051-23	Sequence 23, Appl
2	1291	100.0	1291	14	US-10-090-049-23	Sequence 23, Appl
3	1291	100.0	1291	15	US-10-014-055-23	Sequence 23, Appl
4	1131.6	87.7	1875	9	US-09-903-180B-4	Sequence 4, Appl
5	1131.6	87.7	1875	9	US-09-903-187A-4	Sequence 4, Appl
6	1131.6	87.7	1875	9	US-09-903-171A-4	Sequence 4, Appl
7	1131.6	87.7	1875	9	US-09-903-188A-4	Sequence 4, Appl
8	1131.6	87.7	1875	9	US-09-903-325A-4	Sequence 4, Appl
9	1131.6	87.7	1875	9	US-09-903-325A-4	Sequence 4, Appl
10	1131.6	87.7	1875	9	US-09-903-170C-4	Sequence 4, Appl
11	466.4	36.1	1484	13	US-10-028-051-3	Sequence 3, Appl
12	466.4	36.1	1484	14	US-10-090-049-3	Sequence 3, Appl
13	466.4	36.1	1484	15	US-10-014-055-3	Sequence 3, Appl
14	466.4	36.1	1893	9	US-09-903-180B-10	Sequence 10, Appl
15	466.4	36.1	1893	9	US-09-903-187A-10	Sequence 10, Appl
16	466.4	36.1	1893	9	US-09-903-171A-10	Sequence 10, Appl
17	466.4	36.1	1893	9	US-09-903-188A-10	Sequence 10, Appl
18	466.4	36.1	1893	9	US-09-903-323A-10	Sequence 10, Appl
19	466.4	36.1	1893	9	US-09-903-325A-10	Sequence 10, Appl
20	466.4	36.1	1893	9	US-09-903-170C-10	Sequence 10, Appl
21	466.4	36.1	2039	9	US-09-974-298-16	Sequence 16, Appl
22	466.4	36.1	2625	16	US-10-062-674-1395	Sequence 1395, Ap
23	464.8	36.0	1476	15	US-10-172-118-614	Sequence 614, App
24	464.8	36.0	1476	16	US-10-342-887-614	Sequence 614, App
25	464.8	36.0	1909	10	US-09-960-706-989	Sequence 989, App
26	464.8	36.0	1909	10	US-09-873-319-645	Sequence 645, App
27	464.8	36.0	1909	10	US-09-873-367C-282	Sequence 282, App
28	462	35.8	2176	9	US-09-903-180B-8	Sequence 8, Appl
29	462	35.8	2176	9	US-09-903-187A-8	Sequence 8, Appl
30	462	35.8	2176	9	US-09-903-171A-8	Sequence 8, Appl
31	462	35.8	2176	9	US-09-903-188A-8	Sequence 8, Appl
32	462	35.8	2176	9	US-09-903-323A-8	Sequence 8, Appl
33	462	35.8	2176	9	US-09-903-325A-8	Sequence 8, Appl
34	462	35.8	2176	9	US-09-903-170C-8	Sequence 8, Appl
35	452	35.0	2374	13	US-10-028-051-1	Sequence 1, Appl
36	452	35.0	2374	14	US-10-090-049-1	Sequence 1, Appl
37	452	35.0	2374	15	US-10-014-055-1	Sequence 1, Appl
38	244.2	18.9	1988	14	US-10-208-408-28	Sequence 28, Appl
39	241	18.7	1443	16	US-10-610-917-1	Sequence 1, Appl
40	241	18.7	2820	15	US-10-301-822-188	Sequence 188, App
41	241	18.7	2820	15	US-10-285-027-63	Sequence 63, Appl
42	241	18.7	2820	15	US-10-295-027-960	Sequence 960, App
43	241	18.7	2820	18	US-10-473-974-204	Sequence 204, App
45	241	18.7	2839	9	US-09-909-775-1	Sequence 1, Appl

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OM nucleic - nucleic search, using nw model

Run on: January 10, 2005, 11:50:10 ; Search time 3683.7 Seconds
(without alignment)
12770.772 Million cell updates/sec

Title: US-10-028-051A-23
Perfect score: 1291
Sequence: 1 ttactgtgcagctctccc.....agcctatcatctgatacta 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_eest1:*
2: gb_eest2:*
3: gb_hnc:*
4: gb_eest3:*
5: gb_eest4:*
6: gb_eest5:*
7: gb_eest6:*
8: gb_gnol:*
9: gb_gnol2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	770.6	59.7	851	5	B0908005	B0908005 AGENCOURT
2	698.6	54.1	885	6	CA988226	CA988226 AGENCOURT
3	662.6	51.3	923	5	B0906569	B0906569 AGENCOURT
4	592.2	45.9	702	5	BX853989	BX853989 BX853989
5	524.2	40.6	745	6	CF284632	CF284632 AGENCOURT
6	495.2	38.4	736	7	CK653921	CK653921 AGENCOURT
7	480.6	37.2	929	5	BX755490	BX755490 BX755490
8	466.4	36.1	1305	3	CR593578	CR593578 full-leng
9	466.4	36.1	1780	3	CR620543	CR620543 full-leng
10	466.4	36.1	1891	3	CR622855	CR622855 full-leng
11	462	35.8	2390	3	AK019093	AK019093 Mus muscu
12	462	35.8	2922	3	AK029941	AK029941 Mus muscu
13	453.6	35.1	1001	1	AL548498	AL548498 AL548498
14	451.4	35.0	1032	1	AL546734	AL546734 AL546734
15	447.6	34.7	1159	1	AL515416	AL515416 AL515416
16	446.6	34.6	940	5	BU409451	BU409451 603157994
17	434.6	33.7	882	5	BX758011	BX758011 BX758011
18	430	33.3	891	6	CD105319	CD105319 AGENCOURT
19	423.4	32.8	1094	1	AL528836	AL528836 AL528836
20	418.2	32.4	835	5	B0910785	B0910785 AGENCOURT
21	418.2	32.4	960	7	CF591381	CF591381 AGENCOURT
22	411.2	31.9	928	1	AL527859	AL527859 AL527859
23	409.8	31.7	688	4	B0618816	B0618816 B0618816
24	396.2	30.7	1700	6	CB417263	CB417263 STR00740
25	393.6	30.5	797	9	AY410030	AY410030 Mus muscu
26	392	30.4	797	9	AY410028	AY410028 Homo sapi
27	377.4	29.2	482	1	AL800329	AL800329 AL800329
28	372.8	28.9	750	6	CF284909	CF284909 AGENCOURT
29	365.2	28.3	797	6	CF284587	CF284587 AGENCOURT
30	357.8	27.7	649	4	B0033833	B0033833 B0033833
31	357.8	27.7	651	4	B0625268	B0625268 B0625268
32	354.4	27.5	1065	7	U69182	U69182 U69182 Soar
33	353.6	27.4	759	7	CN083539	CN083539 EC2BBA22D
34	353.6	27.4	805	4	B1769191	B1769191 603060007
35	349.4	27.1	850	6	CF220920	CF220920 AGENCOURT
36	349	27.0	910	6	CF220920	CF220920 AGENCOURT
37	348.6	27.0	651	2	AW318973	AW318973 un10b10.Y
38	348	27.0	991	1	AL526385	AL526385 AL526385
39	346.6	26.8	797	9	AY410029	AY410029 Pan trogl

C	40	345.2	26.7	792	5	BX762262	BX762262
	41	343.8	26.6	889	7	COS58209	AGENCYCOURT
	42	342	26.5	1043	5	BX459201	BX459201
	43	337.2	26.1	787	1	AU141161	AU141161
	44	334.6	25.9	678	2	AW160750	au75f01.y
	45	332.6	25.8	680	4	BI761532	BI761532 603046682